

10/506877

1/13

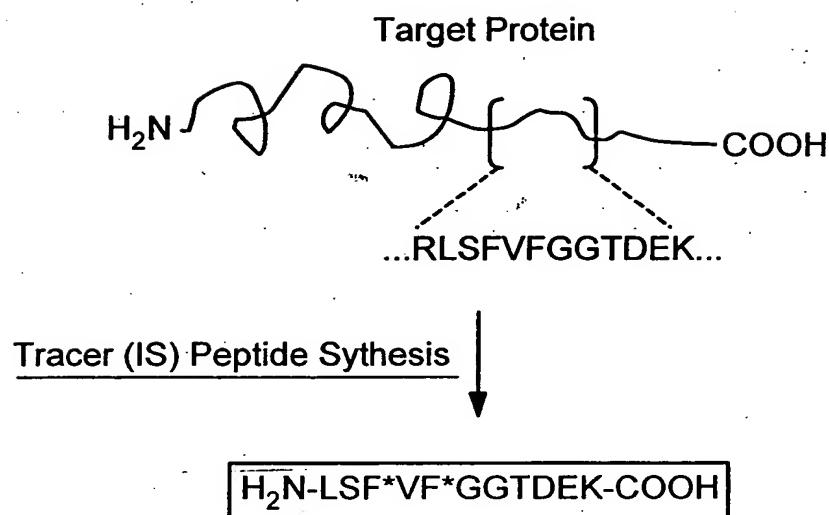


FIG. 1

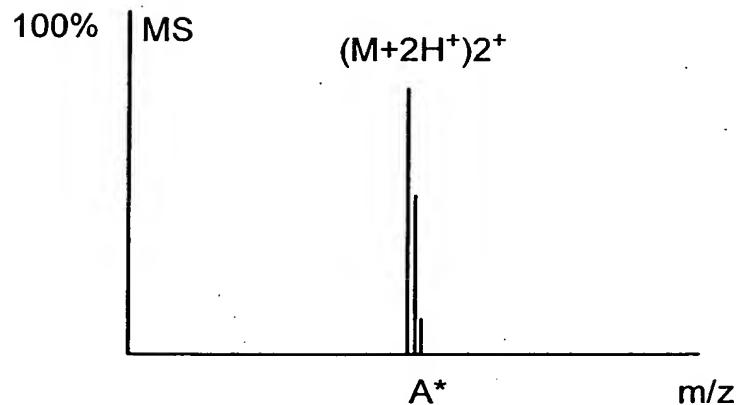


FIG. 2

101506877

Mass Spec of 87% 13C Acetone

2/13

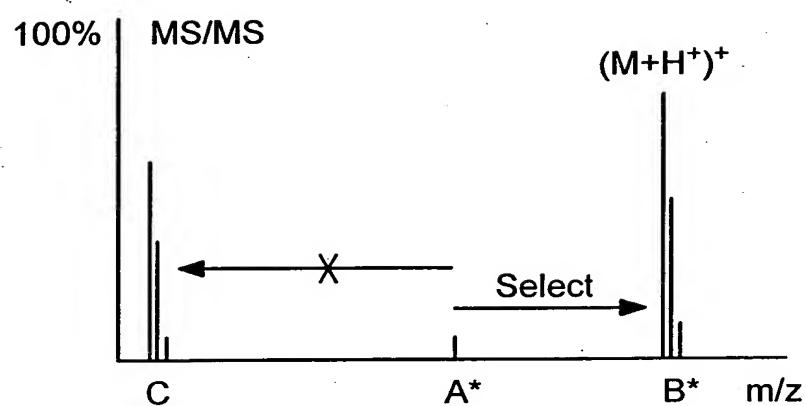


FIG. 3A

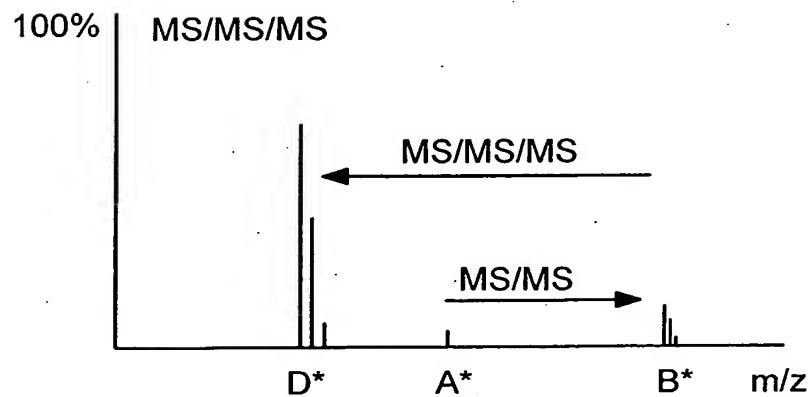


FIG. 3B

3/13

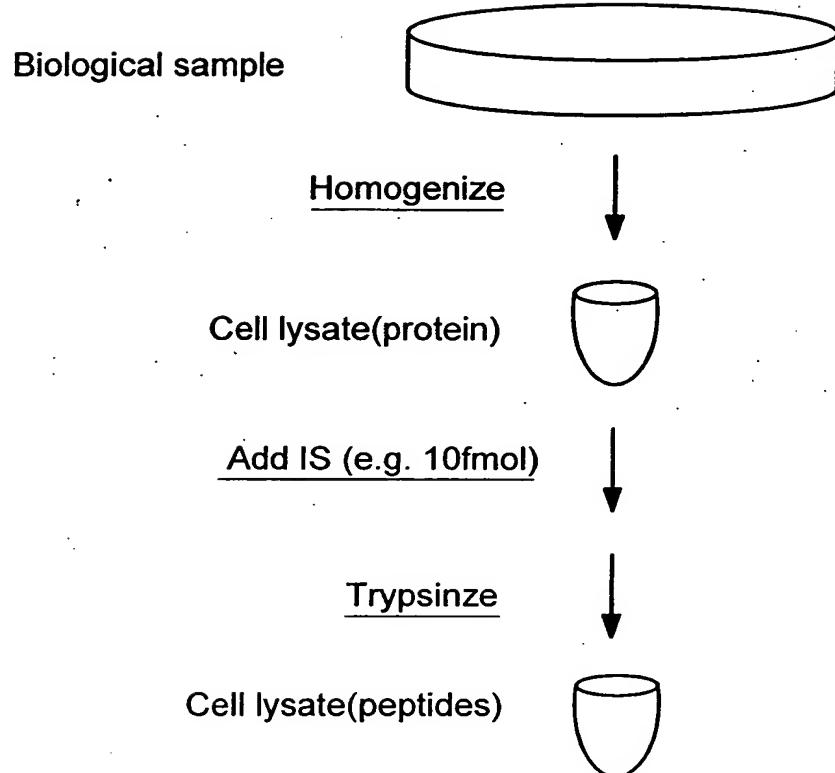


FIG. 4A

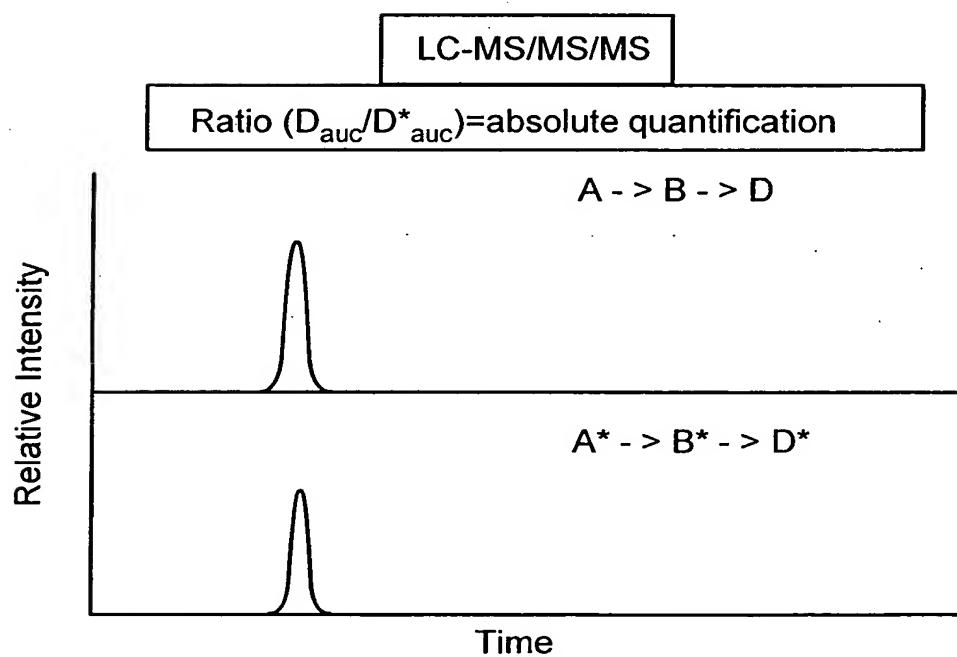
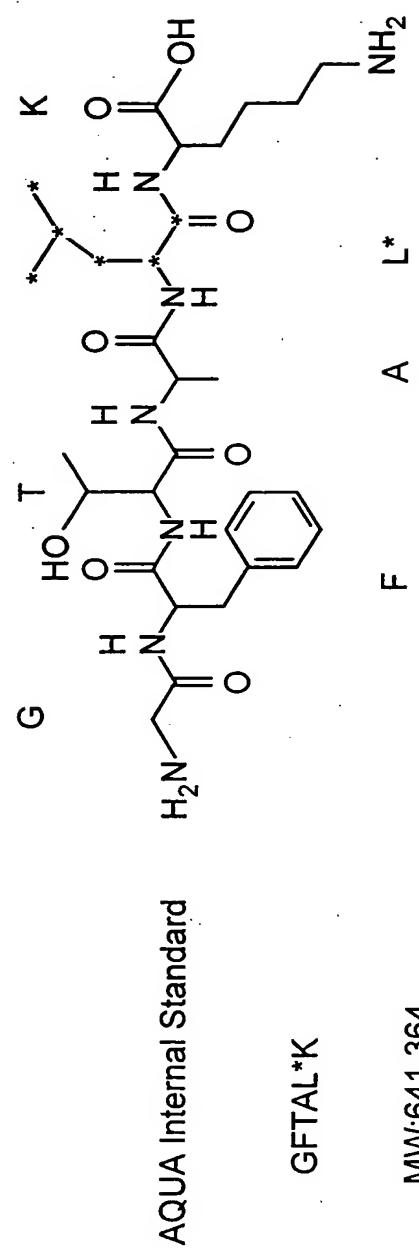
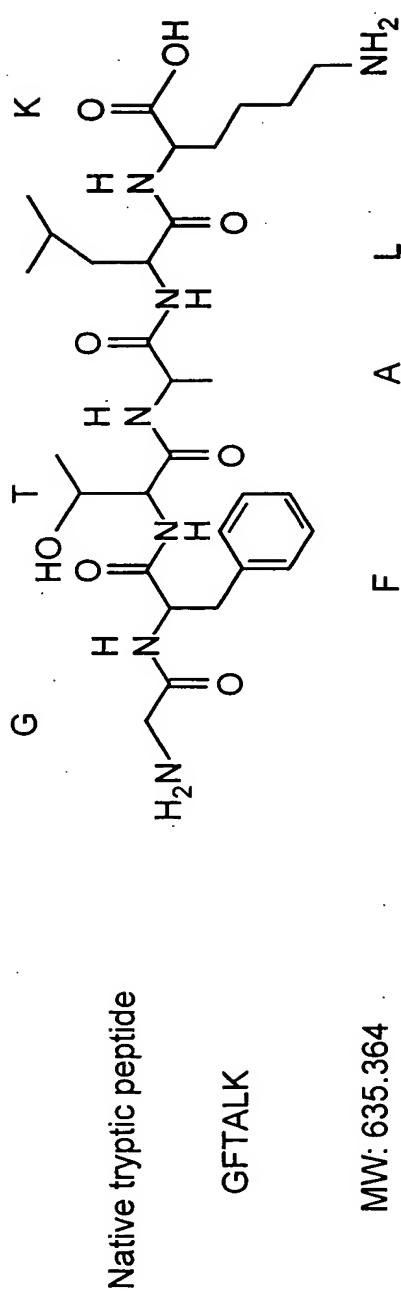


FIG. 4B

101506877

4/13



* = stable isotope (e.g. ^{13}C)

FIG. 5A

5/13

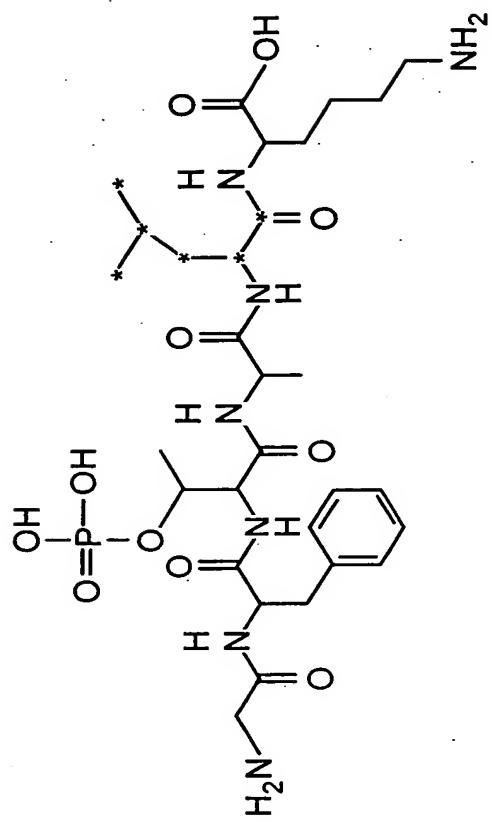
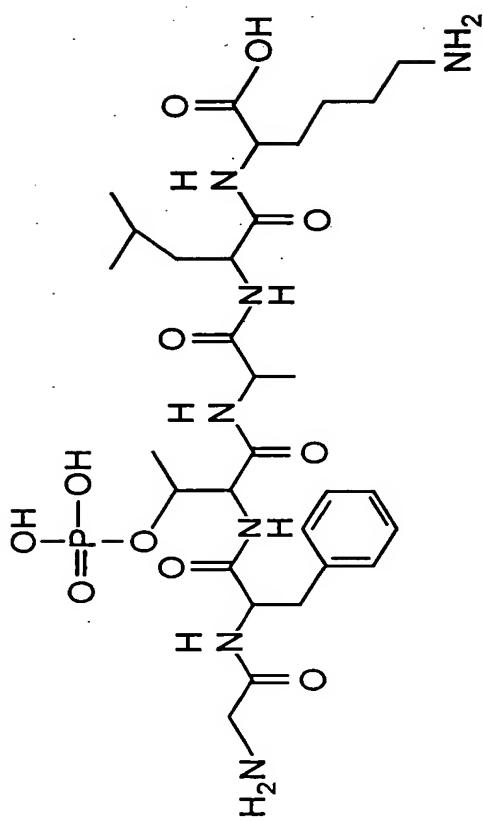
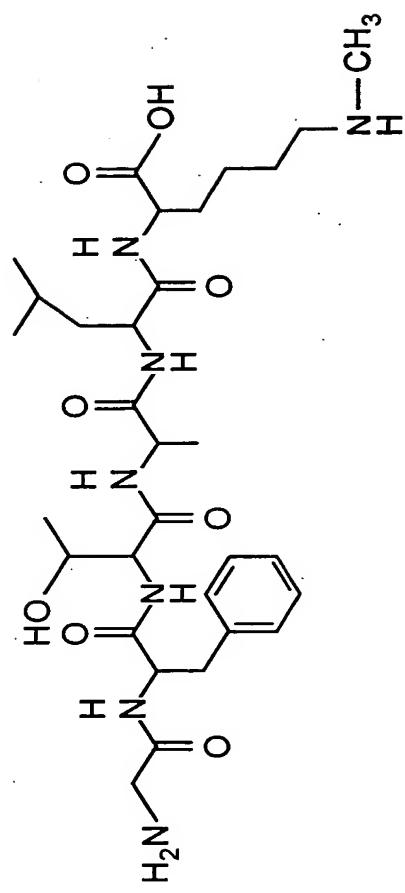


FIG. 5B

* = stable isotope (e.g. ^{13}C)

101506877

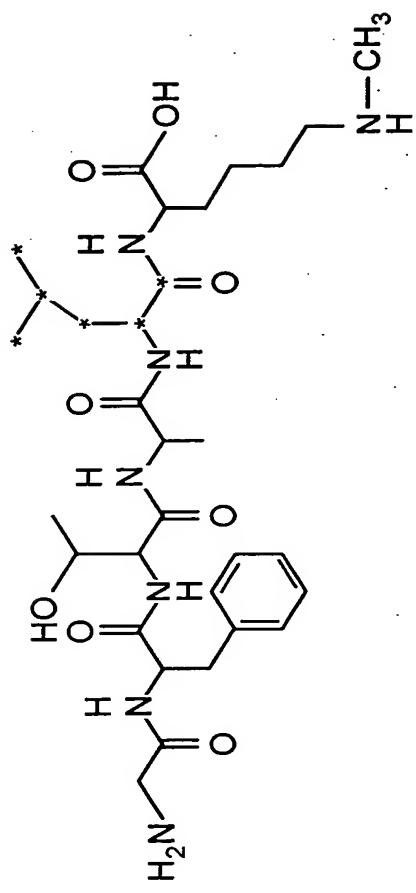
6/13



Native methylated peptide

GFTAL(mK)

MW: 649.79



**AQUA methylated peptide
Internal Standard**

GFTAL*(mK)

MW:655.79

* = Stable isotope (e.g. ^{13}C)

FIG. 5C

101506877

7/13

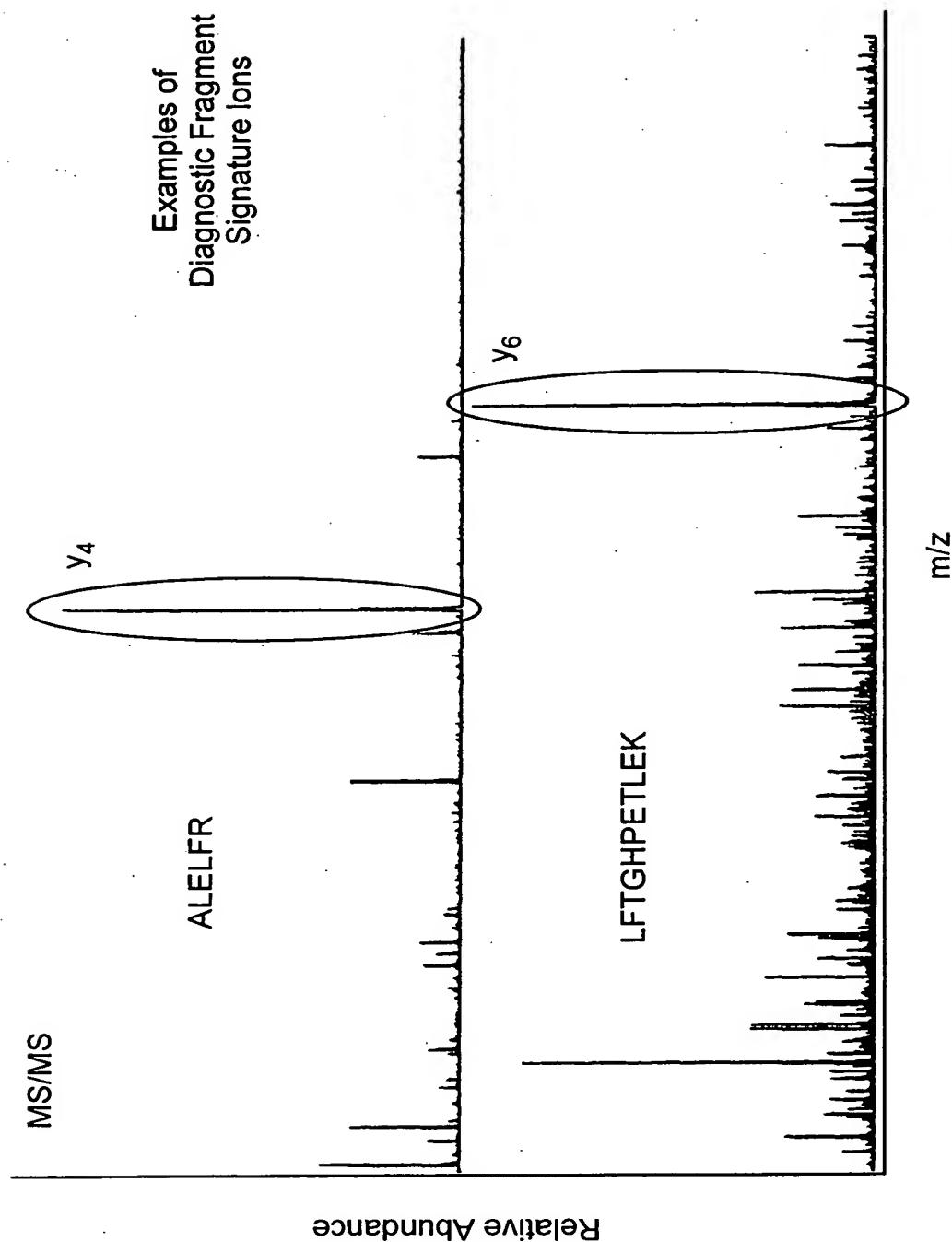


FIG. 6

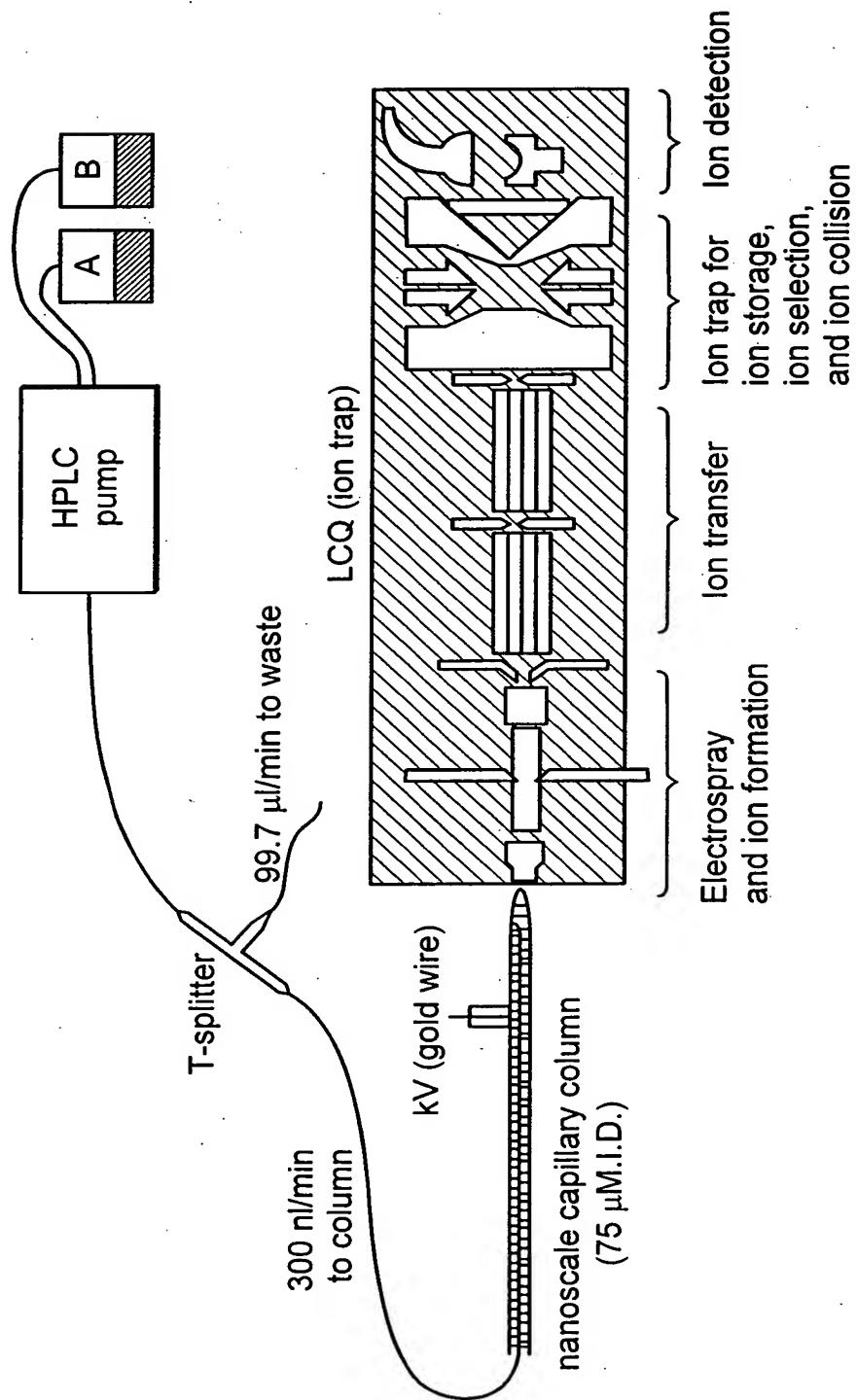


FIG. 7

9/13

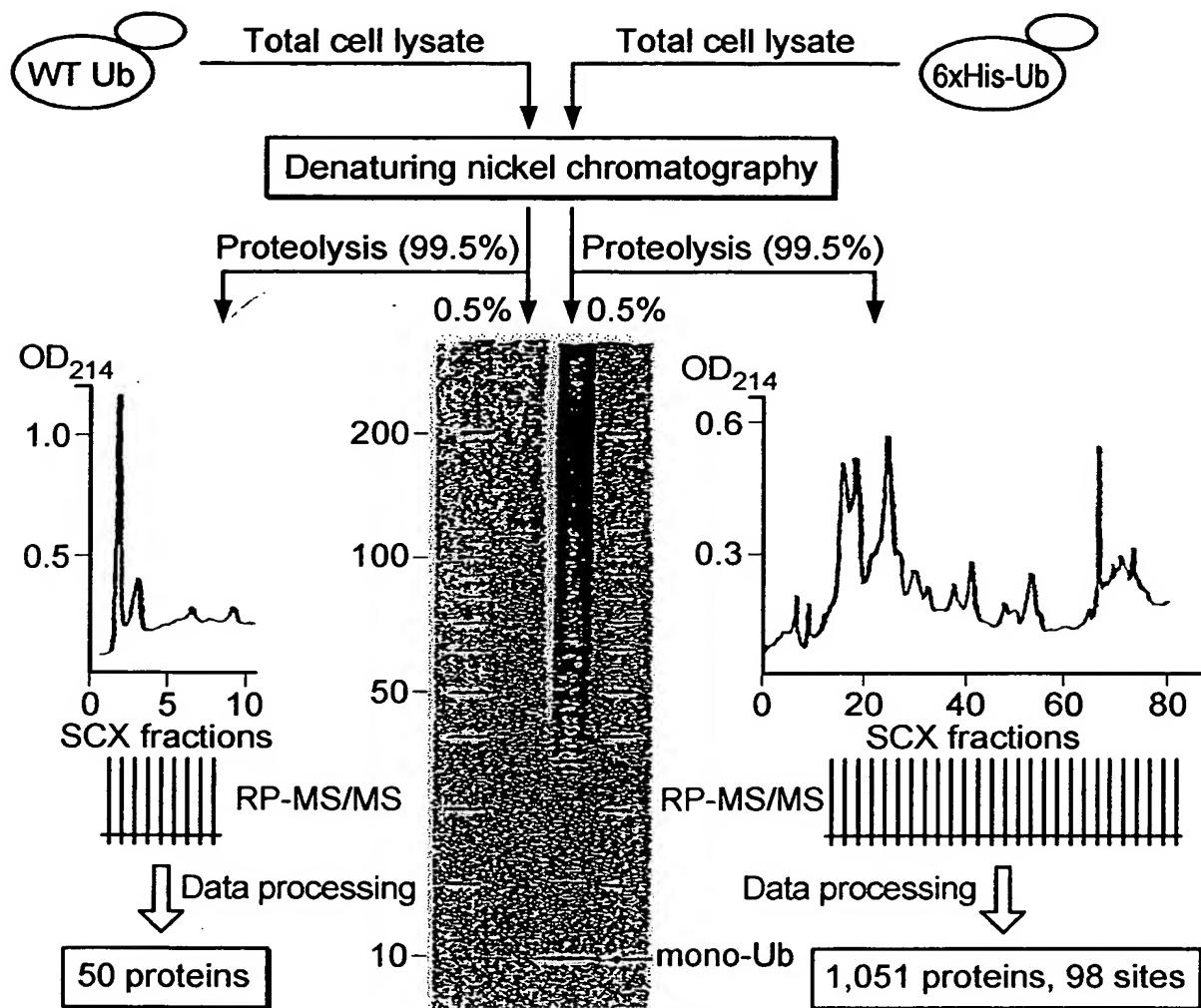


FIG. 8

BEST AVAILABLE COPY

10/506877

10/13

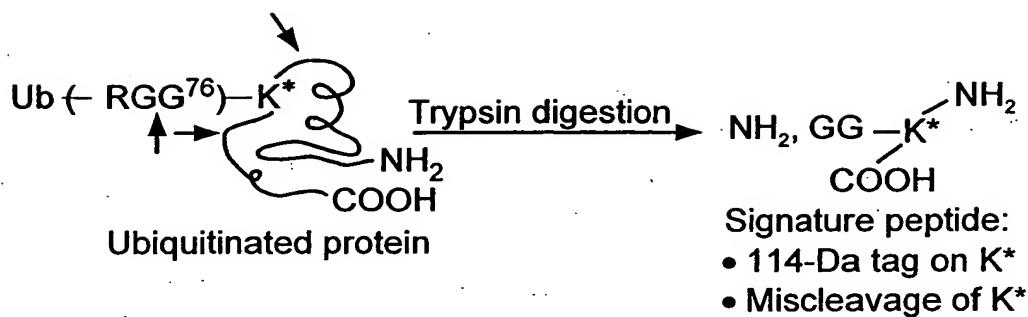


FIG. 9A

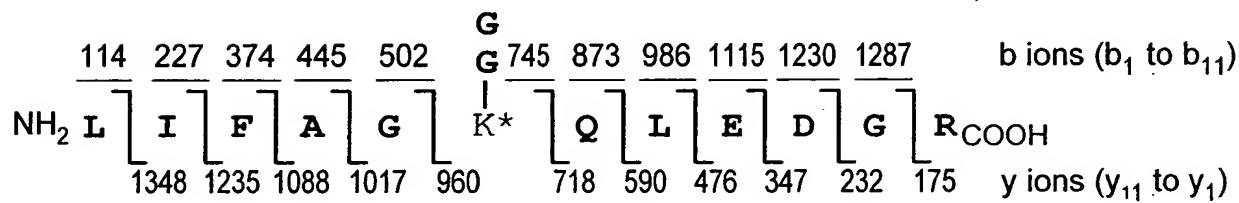


FIG. 9B

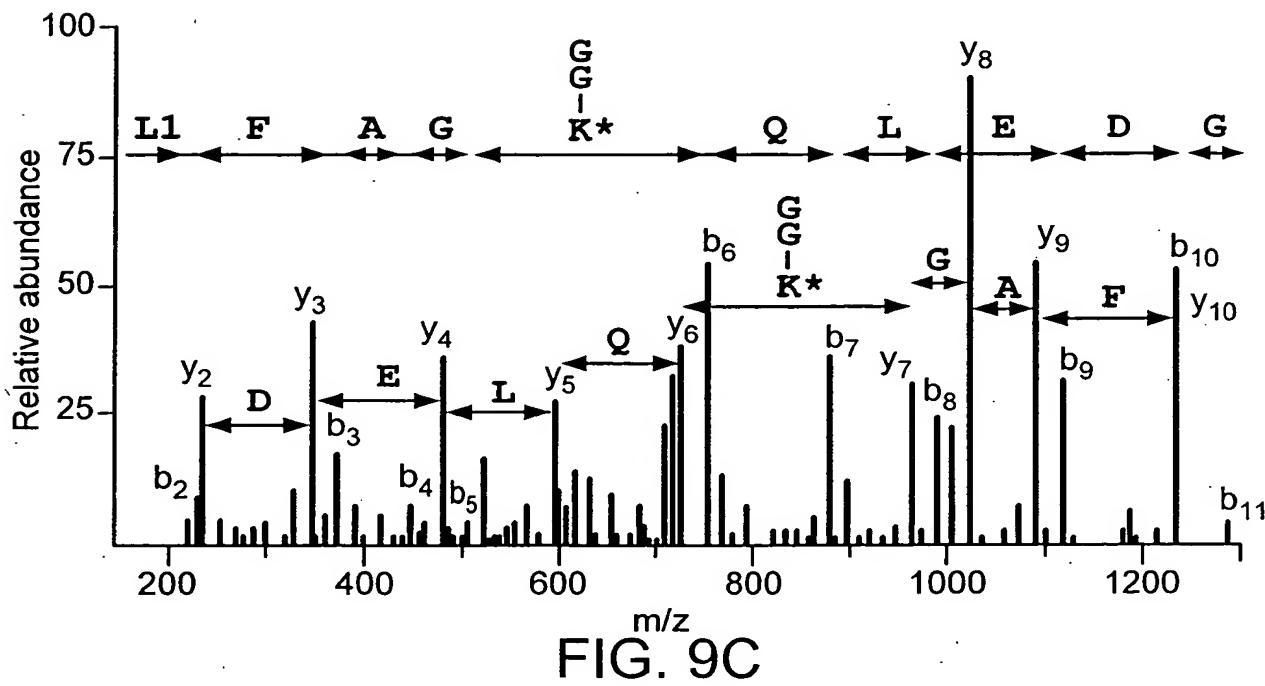


FIG. 9C

10/506877

11/13

Name	#sites	Sequence
Ubiquitin	5	MPFITSRPVA KNSSHSLSET DLNQSKGQPF QPSPTKKLGS MQQRRRSSTI RHALSSLGG
ECM21	5	ANVHSPAVLN NTTKGGNNNG NIRSSNIDAQ LLGKKQNKCP PPNARRHSTT AIQGSISDSA
SAM2	4	TTTPRSSTSD TNRRRTSGRLS VDQEPRISGG RYSQIEEDST VLDFFDDHNS SAVVSSDLSS
YHRD97C	3	TSLTRIANSK KFNEQFLIEY LTARGLLGPK TVLSNEYLKI SISTSGESVF LPTISSNDE
HXT7	3	YLSRLNGLND GTDDAEADFF MDGIDQQEGN TPSLATTAAA TESGGSINEN RDTLLRENNNS
GNP1	3	GDHPGSGSEL NTRSVEIDSS MVSYSIAVIV SVKKPTRFTD MQLELCSRVK VFVNTGVPP
YILD41W	2	KTFNEEFYNA ASMKVNLNDE NFDFLVPLSI SPDQGMIENN SNDRQVRLFK NIPTEERLYL
YHLD1DC	2	DKTKTKASLL NAIDVNKTHL YQPGDYVFLV PVVFSNHIPE TIYLPSARVS YRLRLATKAI
LSB1	2	NRKGFYRQDS NSPQPIVSPD SSSSLSSTTS SLKLTETESA QAHRRISNTL FSKVKNHLHM
ZE01	2	SSHQLNEES GEEDIFAEYP IKVIRTPPPV AVSTANKPIY INRVWTDSLS YEISFAQKYV
PHOM	2	SLNSEVPIKI KLAICKNVC VKRIHVSITE RVTFVSKGYE YEYDQITPVA KDPYNPYYLD
URA3	2	FASKRRKERS VSLFEIRTKE KGTRALREEI VENSFNINLE SYSPFDDSD SKGNPKERLG
GDH1	2	ITEPIIIETK LKFPKYEDLD KRTAKIIPPY GIDAYTSIPN PEHAVANGPS HRRPSVIGFE
ERG5	2	SGHKGSKSHE ENEKPVYDPK FHQDIIKSNS GLPVKTHTRL NIPKRGLYLD SLHFSNVYCR
ERG3	2	HKLEIMIRIS KPDPECPSKL RHYEVLIIDTP IFLVSEQGNS GNMELPTYDM ATMEGKGNQV
YGR26DC	2	PLSMNSDFFG NICPPPPTFE EAISVPASPI VSPMGSPNIM ASYDPDLLSI QQLNLSRTTS
YMR295C	2	VSGPSGYSDD AGVPNVNRNS ISNANAMNGS ISNSAFVSGN SGQGVARARA TSVNDRSRFN
		NLDKLLSTPS PVNRSHNSSP TNGLSQANGT VRIPNATTEN SKDKQNEFFK KGYTLANVKD
		DEEQEGIVSS SSADSLLSHG NEPPRYDEIV PLMSDEE

FIG. 10A

Site in Ub (K)	Signature peptide	SCX fraction	Abundance
48	LIFAGK*QLEDGR	48-56 (9)	high
63	TLSDYNIQK*ESTLHLVLR	65-72 (8)	high
11	TLTGK*TITLEVESSDTIDNVK	38-42 (5)	medium
27	TITLEVESSDTIDNVK*SK	41 (1)	low
6	LISEEDLGMQIFVK*TLTGK	38 (1)	low

FIG. 10B

10/506877

12/13

Name	Phosphopeptide sequence	Description of function
ACC1	AVS*VSDLSYVANSQSSPLR	Acetyl-CoA carboxylase
CCC1	GSGGTSELGGSEST*PLLR	Protein potentially in calcium regulation
CHO1	DENDGYAS*DEVGGLTLSR	Phosphatidylserine synthase
CHS1	DDEYDDLNT*IDK	Chitin synthase I
CHS3	NPSTLLPTS*SMFWNK	Chitin synthase III
ECM21	NEES*GEEDIFAEYPIK HALSS*LLGGANVHSPAVLNNTTK RPS*VIGFLSGHK S*HNSS*PTNGLSQANGTVR	Protein possibly in cell wall biosynthesis
GCD6	EEIDS*EFEDEDFEK	Translation initiation factor eIF2B
HSP3D	ASGETAIHEPEPEAEQAVEDT*A	Heat shock protein located in cell membrane
LYP1	LQVVSHET*DINEDEEEAHYEDK	High affinity lysine specific permease
MET4	KYS*DNEDEYDDADLHGFEK	Transcriptional activator
MYO3	RGS*VYHVPLNPVQATAVR	Myosine type I
PHO84	IHD*T*S*DEDMAINGLER NNDIESSS*PSQLQHEA	Inorganic phosphate/H ⁺ symporter
RAD16	SVYNNELS*DDDTAVK	Nucleotide excision repair protein
Ubiquitin	TLS*DYNIQK	Protein for posttranslational modification
YDR119W	IEEINENS*PLLSAPSK	Member of major facilitator superfamily (MFS)
YDR348C	TNS*FDMPQLNTR	Protein of unknown function
YHR097C	ETVDDDSET*LNQLQDR LPSYEEAGT*PK	Protein of unknown function
YOR042W	KNPDEDEFLINS*DDEM SSGIDEDEVVT*PAEDAKEEEEHHPLPAR EQHHEDS*EEEDSWSQFVEK	Protein of unknown function
YPL019C	HYIADLEDHES*S*DEEGTALPK	Vacuolar polyphosphate accumulation

FIG. 10C

13/13

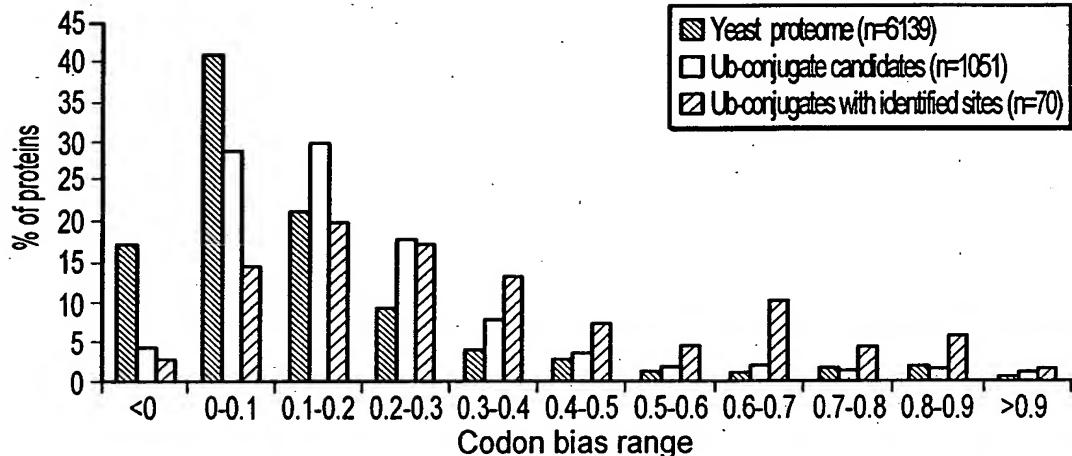


FIG. 11A

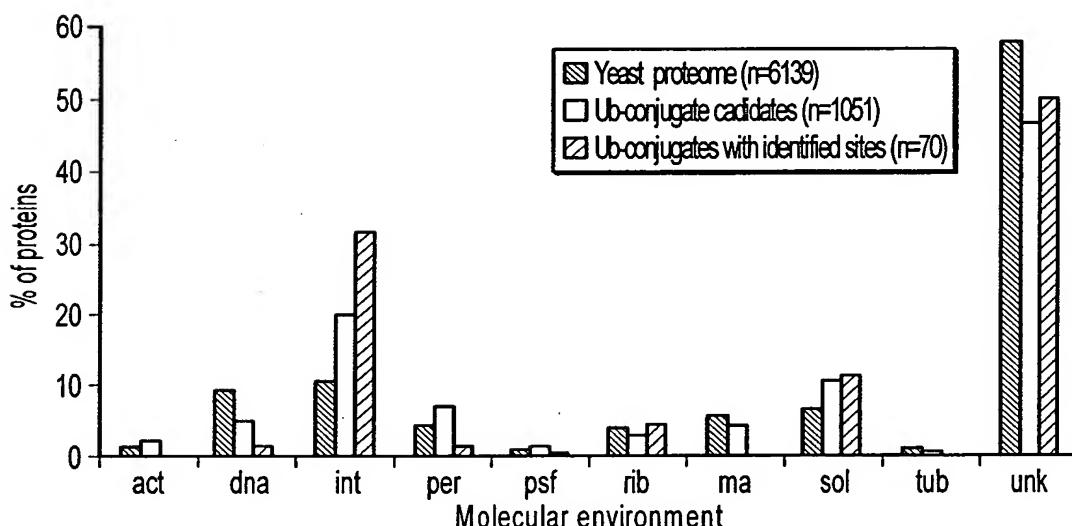


FIG. 11B

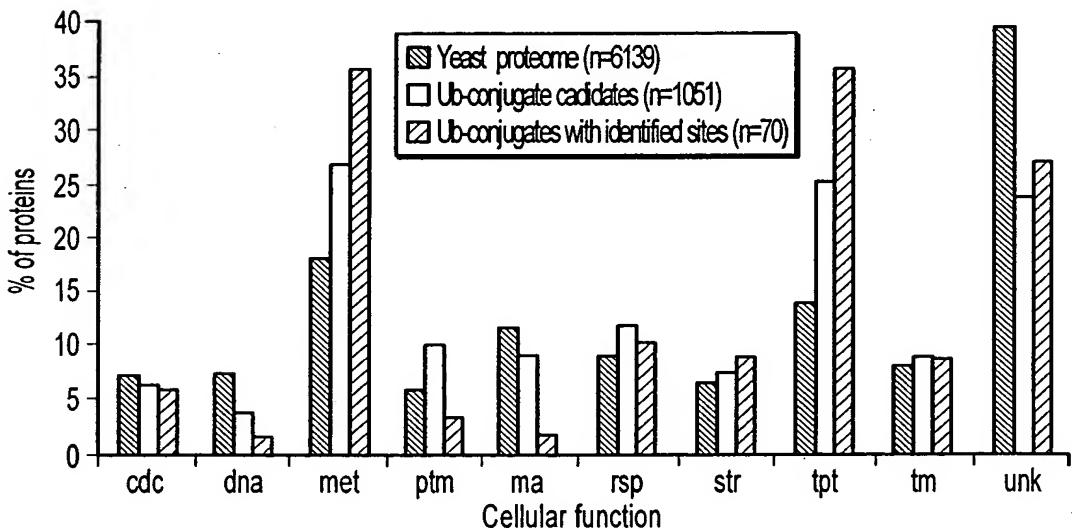


FIG. 11C